

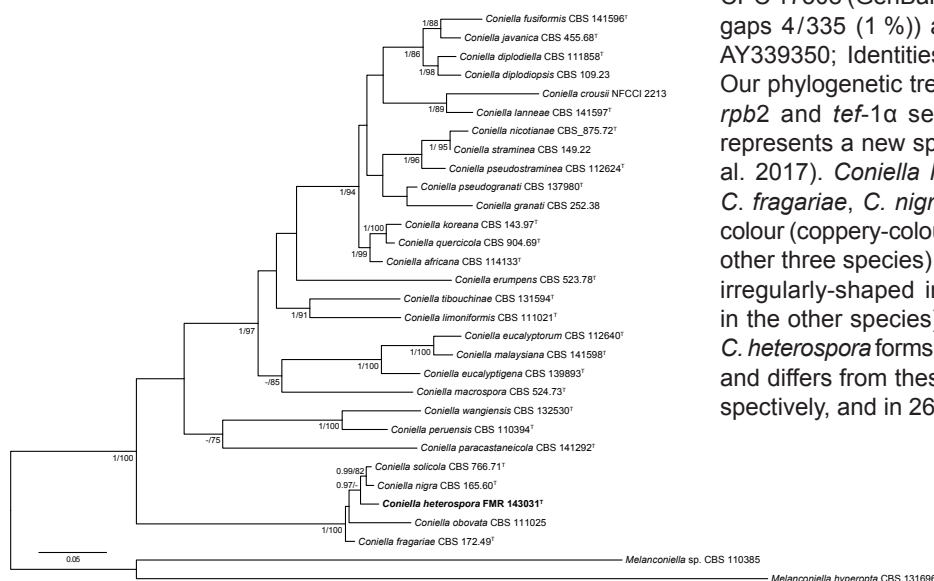
Coniella heterospora



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Coniella heterospora* Valenzuela-Lopez, Cano, Guarro & Stchigel, sp. nov.Etymology.* Named after the variable shape of the conidia.Classification — *Schizoparmaceae*, *Diaporthales*, *Sordariomycetes*.

Hyphae hyaline to pale brown, smooth- and thin- to thick-walled, septate, 2–5 µm wide. *Pycnidia* initially hyaline, becoming dark brown with age due to the production of conidia, glabrous, semi-immersed or superficial (OA), solitary, confluent with age, globose, (320–)370–500(–800) µm diam, without neck, ostiolate, pycnidial wall of *textura angularis*, 50–65 µm thick, 5–6-layered, composed of hyaline to pale brown or brown, flattened polygonal cells of 5–15 µm diam, on the inside of the pycnidium there is a basal central cushion-like structure composed of hyaline cells from which the conidiophores arise. *Conidiophores* densely aggregated, hyaline, branched at the base and with 2–3 supporting cells, or reduced to a single conidiogenous cell. *Conidiogenous cells* hyaline, determinate, smooth- and thin-walled, lageniform, 6.5–12(–16) × 1.5–2(–2.5) µm, 1–1.5 µm wide at apex. *Conidia* hyaline at first, becoming coppery-coloured when mature, aseptate, smooth- and thin- to thick-walled, mostly with a large guttula, sometimes biguttulate, variable in shape, mostly ellipsoidal, sometimes naviculate, limoniform, subsphaerical or irregularly-shaped, mostly laterally compressed, apex acute to nearly rounded, truncate at the base, with a longitudinal germ slit in older conidia, with a minute basal appendage formed by rests of the conidiogenous cell, (4.5–)5.5–8(–9.5) × (3–)4.5–6(–6.5) × 4–4.5(–5.5) µm.



Colour illustrations. Los Cabezudos-Los Bodegones, Huelva, Spain; colony on MEA and OA after 14 d at 25 ± 1 °C; pycnidia under the stereomicroscope; conidiophores, conidiogenous cells and conidia; conidia, some of them showing minute basal cellular appendage (indicated by arrows). Scale bars: conidiophores = 20 µm, conidiogenous cells and conidia = 10 µm..

Culture characteristics — Colonies on OA reaching 79 mm diam after 7 d at 25 ± 1 °C, flattened, white (M. 4A1); reverse white (M. 4A1). Colonies on MEA reaching 86 mm diam after 7 d at 25 ± 1 °C, floccose, brownish grey (M. 4D2) to dark grey (M. 4F1); reverse dark grey (M. 4F1). NaOH spot test negative. Crystals absent. Optimal temperature of sporulation and growth, 25 °C; minimum temperature of growth, 15 °C; maximum temperature of growth, 30 °C.

Typus. SPAIN, Huelva, Almonte, road HF6245 from Los Cabezudos village to Los Bodegones village, from herbivorous dung, Mar. 2016, coll. C. González-García and G. Sisó, isol. N. Valenzuela-Lopez (holotype CBS H-23198, cultures ex-type FMR 15231 = CBS 143031, ITS, LSU, *tef-1α* and *rpb2* sequences GenBank LT800501, LT800500, LT800503 and LT800502, MycoBank MB820451).

Notes — *Coniella heterospora* is characterised by the production of coppery-coloured conidia that are variable in shape. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hit using the LSU sequence is *C. fragariae* CBS 183.52 (GenBank KJ710442; Identities = 835/838 (99 %), no gaps). Closest hits using the ITS sequence are *C. fragariae* CBS 198.82 (GenBank KJ710465; Identities = 600/601 (99 %), no gaps) and *C. solicola* CPC 17308 (GenBank KX833598; Identities = 589/591 (99 %), no gaps). The closest hits using the *rpb2* sequence are *C. solicola* CBS 114007 (GenBank KX833504; Identities = 756/767 (99 %), no gaps) and *C. fragariae* CBS 454.68 (GenBank KX833477; Identities = 751/767 (98 %), no gaps). The closest hits using the *tef-1α* sequence are *C. solicola* CPC 17308 (GenBank KX833702; Identities = 311/335 (93 %), gaps 4/335 (1 %)) and *C. fragariae* STE-U 3713 (GenBank AY339350; Identities = 327/359 (91 %), gaps 9/359 (2 %)). Our phylogenetic tree, built by using concatenated LSU, ITS, *rpb2* and *tef-1α* sequences, corroborated that our isolate represents a new species (Alvarez et al. 2016, Marin-Felix et al. 2017). *Coniella heterospora* is morphologically similar to *C. fragariae*, *C. nigra* and *C. solicola*, but differs in conidium colour (coppery-coloured in *C. heterospora* vs dark brown in the other three species) and shape (very variable and sometimes irregularly-shaped in *C. heterospora*, and scarcely variable in the other species). The phylogenetic analysis showed that *C. heterospora* forms a basal branch with *C. solicola* and *C. nigra*, and differs from these species in 8 bp and 10 bp for *rpb2*, respectively, and in 26 bp for both *tef-1α* nucleotide sequences.

Maximum likelihood tree obtained from the combined DNA sequences dataset from four loci (LSU, ITS, *rpb2* and *tef-1α*) of our isolate and sequences retrieved from the GenBank database. Ex-type strains of the different species are indicated with †. The new species proposed in this study is indicated in **bold**. The Bayesian posterior probabilities (≥ 0.95) and RAxML bootstrap support values (≥ 70 %) are provided at the nodes. *Melanconiella hyperopta* CBS 131696 and *Melanconiella* sp. CBS 110385 were used as outgroup.

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